Chapter XII
Distributed Medical Volume Registration

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ABSTRACT

The registration of corresponding patient volumes is often a pre-requisite for medical imaging tasks. Accurate alignment, however, usually results in high computational complexity and can hence take a considerable amount of time. This is particularly true with 3-D volume data which adds another dimension to the registration process. One possibility of keeping registration times feasible is to distribute computation among several processors so that it maybe accomplished in parallel. This chapter provides a short survey of parallel registration approaches which have been proposed together with some recent research adopting a blackboard architecture for distributed high performance image and volume registration purposes.

INTRODUCTION

The ability to visualise hidden structures in detail using 3-D volume data has become a valuable resource in medical imaging applications (Maintz & Viergever, 1998). Importantly, the alignment of volumes enables the combination of different structural and functional information for diagnosis and planning purposes (Pluim, Maintz, & Viergever, 2003). Transform optimisation,

re-sampling, and similarity calculation form the basic stages of a registration process (Zitova & Flusser, 2003). During transform optimisation, translation and rotation parameters which geometrically map points in the reference (fixed) volume to points in the sensed (moving) volume are estimated. Once estimated, voxel intensities which are mapped into non-discrete co-ordinates are interpolated during the re-sampling stage. After re-sampling, a metric is used for similarity calculation in which the degree of likeness between corresponding volumes is evaluated. Optimisation of the similarity measure is the goal of the registration process and is achieved by seeking the best transform. All possible transform parameters therefore define the search space. Due to the iterative nature of registration algorithms similarity calculation represent a considerable performance bottleneck which limits the speed of time critical clinical applications.

The use of parallel computing to overcome these time constraints has become an important research area (Nicolescu & Jonker, 2000). Conveniently, many of the similarity calculation strategies employed in medical registration are inherently parallel and therefore well suited to distribution. An important consideration when adopting a parallel processing approach is the architecture of the host system. In a computer constructed of multiple processors with shared-memory, data distribution is not required. These systems are viewed as tightly-coupled architectures. In contrast, a loosely-coupled architecture consists of multiple computers in different locations. Loosely-coupled architectures therefore require data distribution, communication, and accumulation mechanisms. Logically, the most effective distribution scheme will depend on the architecture of the host system (Seinstra, Koelma, & Geusebroek, 2002). The two contrasting architectures of host systems are illustrated in Figure 1.

BACKGROUND

In the context of parallel processing, registration of medical data has been achieved by Warfield *et al.* (Warfield, Jolesz, and Kikinis, 1998) who introduced a non-rigid algorithm based on the work-pile paradigm. Their goal was to develop an inter-patient registration algorithm which can be applied without operator intervention, to a database of several hundred scans. In an initial step, each scan is segmented using a statistical classification method. This pre-processing stage

Figure 1. Tightly vs. loosely-coupled architectures. Data is either fetched from main memory via a memory bus, or is transferred over a communications network.